

## **REMARKS**

### **Introductory Comments**

Reconsideration of the above-identified application in view of the foregoing arguments is respectfully requested.

Claims 52-81 are pending. Claims 62-69 and 71-76 remain withdrawn from consideration. Claims 52-61, 70 and 77-81 are under consideration.

### **Rejection of Claims 52-61, 70 and 77-81 Under 35 U.S.C. § 101**

#### **And § 112, First Paragraph**

Claims 52-61, 70 and 77-81 are rejected under 35 U.S.C. § 101 and § 112, first paragraph, for the reason contained in the previous Office Action. The Examiner contends that the Declaration of Dr. Granados is germane to the rejection at issue and that it fails to provide any evidence that the BS322 polypeptides according to SEQ ID NOS: 25-28 are equivalent to the NY-BR-1 breast cancer antigen polypeptide. Applicants respectfully traverse this rejection.

As submitted by Applicants in their previous responses, the Dirk Jager *et al.* article "Identification of Tissue-specific Putative Transcription Factor..." support Applicants' contention that SEQ ID NOS: 24-28 as claimed are useful as required by 35 U.S.C. § 101 and § 112, first paragraph. The Jager *et al.* article shows that the gene NY-BR-1 is one of the genes responsible for breast cancer. The gene has 37 exons. See the abstract. Applicants have shown in previous responses in Exhibit A, the 100% alignment match and homology between NY-BR-1 and a nucleotide sequence designated BS322 (SEQ ID NO: 9). Nucleotide sequence BS322 or SEQ ID NO: 9 as described in the instant specification, encodes the polypeptide sequences designated SEQ ID NOS: 24-28. These polypeptides are useful in the detection of breast disease which Examiner has refuted.

The Examiner contends in the previous Office Actions that the alignment match between BS322 and NY-BR-1 does not prove that BS322 is the same molecule as NY-BR-1 since 1143 nucleotides are unaccounted for. The Examiner uses this single basis to support her reason why SEQ ID NOS: 24-28 are not useful in the detection of breast disease. Although Applicants appreciate the Examiner's detailed analysis, Applicants respectfully traverse the rejection and contend this line of reasoning is flawed for the reason set forth below.

Applicants agree with the Examiner's observation that the alignment consensus between BS322 and NY-BR-1 does not prove BS322 is the exact same molecule of NY-BR-1. However, the 100% consensus between these two molecules over one thousand nucleotides indicates that BS322 could be a splice variant of NY-BR-1. Applicants have attached herein a portion of a BLAST result for AF269087 (NY-BR-1) versus the human genome. As the Examiner can see, the junctions of the exons for the gaps match those that are in the BS322 molecule. Specifically, three exons that account for gaps are at the positions of 3013-3200, 3197-4116 and 2796-3014. This information clearly provides evidence that BS322 is a splice variant of NY-BR-1.

As indicated in the Jager *et al.* article, NY-BR-1 comprises 37 exons. Exons, also known as expressed sequences, are defined as a portions of a gene

that appear in both the primary and mature mRNA transcripts (Fundamentals of Biochemistry, Voet *et al.*, John Wiley & Sons, Inc., 1999). Thus, one of ordinary skill in the art would recognize that although BS322 is not the exact molecule of NY-BR-1, the fact that there is a 100% consensus homology between the two molecules for over 1000 nucleotides of the exons indicates that one is a splice of another and would have significant commonalities. It is well known in the art that introns may be excluded from splices which maintain the functionality of a gene. An intron, also called an intervening sequence, is defined in the art as a part of a primary transcript, or DNA encoding it, that is removed by splicing during RNA processing and is not included in the mature, functional mRNA, rRNA or tRNA (Fundamentals of Biochemistry, Voet *et al.*, John Wiley & Sons, Inc., 1999).

As disclosed in the specification, SEQ ID NOS: 24-28 are derived from the BS322 molecule. As shown in Jager *et al.*, *supra*, and in Applicants' disclosure, mRNA expressions of the gene, i.e., sequence segments from the genes which encode proteins that have a specific epitope, are useful as markers for breast diseases. Thus, for these reasons, Applicants respectfully request the Examiner to withdraw the rejection of claims 52-61, 70 and 77- 35 under 35 U.S.C. § 101 and § 112, first paragraph, and allow the claims.

## CONCLUSION

Applicants respectfully submit that the claims comply with the requirements of 35 U.S.C. Sections 101, 112, 102 and 103. Accordingly, a Notice of Allowance is believed in order and is respectfully requested.

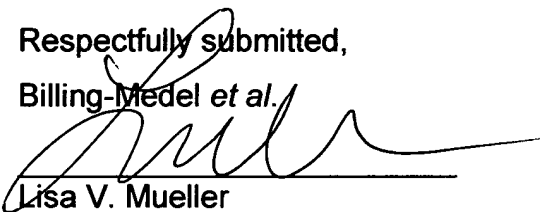
Should the Examiner have any questions concerning the above, she is respectfully requested to contact the undersigned at the telephone number listed below. If the Examiner notes any further matters which the Examiner believes may be expedited by a telephone interview, the Examiner is requested to contact the undersigned.

If any additional fees are incurred as a result of the filing of this paper, authorization is given to charge deposit account no. 23-0785.

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Respectfully submitted,  
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## BS322 Contig summary1.TXT

## Summary View of Contig "Contig[0013]"

>AF269087	#1	CTAGTCTATA CCAGCAACGA CTCCTACATC
	#1	..... CTAGTCTATA CCAGCAACGA CTCCTACATC
>AF269087	#31	GTCCACTCTG GGGATCTTAG AAAGATCCAT
	#31	..... GTCCACTCTG GGGATCTTAG AAAGATCCAT
>AF269087	#61	AAAGCTGCCT CCCGGGGACA AGTCCGGAAG
	#61	..... AAAGCTGCCT CCCGGGGACA AGTCCGGAAG
>AF269087	#91	CTGGAGAAGA TGACAAAGAG GAAGAAGACC
	#91	..... CTGGAGAAGA TGACAAAGAG GAAGAAGACC
>AF269087	#121	ATCAACCTTA ATATACAAGA CGCCCAGAAG
	#121	..... ATCAACCTTA ATATACAAGA CGCCCAGAAG
>AF269087	#151	AGGACTGCTC TACTCTGGGC CTGTGTCAAT
	#151	..... AGGACTGCTC TACTCTGGGC CTGTGTCAAT
>AF269087	#181	GGCCATGAGG AAGTAGTAAC ATTTCTGGTA
	#181	..... GGCCATGAGG AAGTAGTAAC ATTTCTGGTA
>AF269087	#211	GACAGAAAGT GCCAGCTTGA CGTCCTTGAT
	#211	..... GACAGAAAGT GCCAGCTTGA CGTCCTTGAT
>AF269087	#241	GGCGAACACA GGACACCTCT GATGAAGGCT
	#241	..... GGCGAACACA GGACACCTCT GATGAAGGCT
>AF269087	#271	CTACAATGCC ATCAGGAGGC TTGTGCAAAT
	#271	..... CTACAATGCC ATCAGGAGGC TTGTGCAAAT
>AF269087	#301	ATTCTGATAG ATTCTGGTGC CGATATAAAT
	#301	..... ATTCTGATAG ATTCTGGTGC CGATATAAAT
>AF269087	#331	CTCGTAGATG TGTATGGCAA CATGGCTCTC
	#331	..... CTCGTAGATG TGTATGGCAA CATGGCTCTC

## BS322 Contig summary1.TXT

>AF269087	#361	CATTATGCTG TTTATAGTGA GATTTTGTCA
	#361	..... CATTATGCTG TTTATAGTGA GATTTTGTCA
>AF269087	#391	GTGGTGGCAA AACTGCTGTC CCATGGTGCA
	#391	..... GTGGTGGCAA AACTGCTGTC CCATGGTGCA
>AF269087	#421	GTCATCGAAG TGCACAACAA GGCTAGCCTC
	#421	..... GTCATCGAAG TGCACAACAA GGCTAGCCTC
>AF269087	#451	ACACCACTTT TACTATCCAT AACGAAAAGA
	#451	..... ACACCACTTT TACTATCCAT AACGAAAAGA
>AF269087	#481	AGTGAGCAAA TTGTGGAATT TTTGCTGATA
	#481	..... AGTGAGCAAA TTGTGGAATT TTTGCTGATA
>AF269087	#511	AAAAATGCAA ATGCGAATGC AGTTAATAAG
	#511	..... AAAAATGCAA ATGCGAATGC AGTTAATAAG
>AF269087	#541	TATAAATGCA CAGCCCTCAT GCTTGCTGTA
	#541	..... TATAAATGCA CAGCCCTCAT GCTTGCTGTA
>AF269087	#571	TGTCATGGAT CATCAGAGAT AGTTGGCATG
	#571	..... TGTCATGGAT CATCAGAGAT AGTTGGCATG
>AF269087	#601	CTTCTTCAGC AAAATGTTGA CGTCTTTGCT
	#601	..... CTTCTTCAGC AAAATGTTGA CGTCTTTGCT
>AF269087	#631	GCAGATATAT GTGGAGTAAC TGCAGAACAT
	#631	..... GCAGATATAT GTGGAGTAAC TGCAGAACAT
>AF269087	#661	TATGCTGTTA CTTGTGGATT TCATCACATT
	#661	..... TATGCTGTTA CTTGTGGATT TCATCACATT
>AF269087	#691	CATGAACAAA TTATGGAATA TATACGAAAA
	#691	..... CATGAACAAA TTATGGAATA TATACGAAAA
>AF269087	#721	TTATCTAAAA ATCATCAAAA TACCAATCCA
	#721	..... TTATCTAAAA ATCATCAAAA TACCAATCCA

BS322 Contig summary1.TXT

>AF269087	#751	GAAGGAACAT CTGCAGGAAC ACCTGATGAG
	#751	GAAGGAACAT CTGCAGGAAC ACCTGATGAG
>AF269087	#781	GCTGCACCCT TGGCGGAAAG AACACCTGAC
	#781	GCTGCACCCT TGGCGGAAAG AACACCTGAC
>AF269087	#811	ACAGCTGAAA GCTTGGTGGG AAAAACACCT
	#811	ACAGCTGAAA GCTTGGTGGG AAAAACACCT
>AF269087	#841	GATGAGGCTG CACCCTTGGT GGAAAGAACA
	#841	GATGAGGCTG CACCCTTGGT GGAAAGAACA
>AF269087	#871	CCTGACACGG CTGAAAGCTT GGTGGAAAAA
	#871	CCTGACACGG CTGAAAGCTT GGTGGAAAAA
>AF269087	#901	ACACCTGATG AGGCTGCATC CTTGGTGGAG
	#901	ACACCTGATG AGGCTGCATC CTTGGTGGAG
>AF269087	#931	GGAACATCTG ACAAATTCA ATGTTTGGAG
	#931	GGAACATCTG ACAAATTCA ATGTTTGGAG
>AF269087	#961	AAAGCGACAT CTGGAAAGTT CGAACAGTCA
	#961	AAAGCGACAT CTGGAAAGTT CGAACAGTCA
>AF269087	#991	GCAGAAGAAA CACCTAGGGA AATTACGAGT
	#991	GCAGAAGAAA CACCTAGGGA AATTACGAGT
>AF269087	#1021	CCTGCAAAAG AAACATCTGA GAAATTTACG
	#1021	CCTGCAAAAG AAACATCTGA GAAATTTACG
>AF269087	#1051	TGGCCAGCAA AAGGAAGACC TAGGAAGATC
	#1051	TGGCCAGCAA AAGGAAGACC TAGGAAGATC
>AF269087	#1081	GCATGGGAGA AAAAAGAAGA CACACCTAGG
	#1081	GCATGGGAGA AAAAAGAAGA CACACCTAGG
>AF269087	#1111	GAAATTATGA GTCCCGCAAA AGAAACATCT

## BS322 Contig summary1.TXT

	#1111	..... GAAATTATGA GTCCCGCAAA AGAAACATCT
>AF269087	#1141	GAGAAATTTA CGTGGGCAGC AAAAGGAAGA
	#1141	..... GAGAAATTTA CGTGGGCAGC AAAAGGAAGA
>AF269087	#1171	CCTAGGAAGA TCGCATGGGA GAAAAAAGAA
	#1171	..... CCTAGGAAGA TCGCATGGGA GAAAAAAGAA
>AF269087	#1201	ACACCTGTAA AGACTGGATG CGTGGCAAGA
	#1201	..... ACACCTGTAA AGACTGGATG CGTGGCAAGA
>AF269087	#1231	GTAACATCTA ATAAACTAA AGTTTTGGAA
	#1231	..... GTAACATCTA ATAAACTAA AGTTTTGGAA
>AF269087	#1261	AAAGGAAGAT CTAAGATGAT TGCATGTCCT
	#1261	..... AAAGGAAGAT CTAAGATGAT TGCATGTCCT
>AF269087	#1291	ACAAAAGAAT CATCTACAAA AGCAAGTGCC
	#1291	..... ACAAAAGAAT CATCTACAAA AGCAAGTGCC
>AF269087	#1321	AATGATCAGA GGTTCCTATC AGAATCCAAA
	#1321	..... AATGATCAGA GGTTCCTATC AGAATCCAAA
>AF269087	#1351	CAAGAGGAAG ATGAAGAATA TTCTTGTGAT
	#1351	..... CAAGAGGAAG ATGAAGAATA TTCTTGTGAT
>AF269087	#1381	TCTCGGAGTC TCTTTGAGAG TTCTGCAAAG
	#1381	..... TCTCGGAGTC TCTTTGAGAG TTCTGCAAAG
>AF269087	#1411	ATTCAAGTGT GTATACCTGA GTCTATATAT
	#1411	..... ATTCAAGTGT GTATACCTGA GTCTATATAT
>AF269087	#1441	CAAAAAGTAA TGGAGATAAA TAGAGAAGTA
	#1441	..... CAAAAAGTAA TGGAGATAAA TAGAGAAGTA
>AF269087	#1471	GAAGAGCCTC CTAAGAAGCC ATCTGCCTTC
	#1471	..... GAAGAGCCTC CTAAGAAGCC ATCTGCCTTC



## BS322 Contig summary1.TXT

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>AF269087      #1501      AAGCCTGCCA TTGAAATGCA AAACCTCTGT
#1501      AAGCCTGCCA TTGAAATGCA AAACCTCTGT

>AF269087      #1531      CCAAATAAAG CCTTTGAATT GAAGAATGAA
#1531      CCAAATAAAG CCTTTGAATT GAAGAATGAA

>AF269087      #1561      CAAACATTGA GAGCAGATCC GATGTTCCCA
#1561      CAAACATTGA GAGCAGATCC GATGTTCCCA

>AF269087      #1591      CCAGAATCCA AACAAAAGGA CTATGAAGAA
#1591      CCAGAATCCA AACAAAAGGA CTATGAAGAA

>AF269087      #1621      AATTCTTGGG ATTCTGAGAG TCTCTGTGAG
#1621      AATTCTTGGG ATTCTGAGAG TCTCTGTGAG

>AF269087      #1651      ACTGTTTCAC AGAAGGATGT GTGTTTACCC
#1651      ACTGTTTCAC AGAAGGATGT GTGTTTACCC

>AF269087      #1681      AAGGCTACAC ATCAAAAAGA AATAGATAAA
#1681      AAGGCTACAC ATCAAAAAGA AATAGATAAA

>AF269087      #1711      ATAAATGGAA AATTAGAAGA GTCTCCTAAT
#1711      ATAAATGGAA AATTAGAAGA GTCTCCTAAT

>AF269087      #1741      AAAGATGGTC TTCTGAAGGC TACCTGCGGA
#1741      AAAGATGGTC TTCTGAAGGC TACCTGCGGA

>AF269087      #1771      ATGAAAGTTT CTATTCCAAC TAAAGCCTTA
#1771      ATGAAAGTTT CTATTCCAAC TAAAGCCTTA

>AF269087      #1801      GAATTGAAGG ACATGCAAAC TTTCAAAGCG
>BS322 1 to 1198 >#1>      AGTATAC ATTCTTTATT
#1801      GAATTGAAGG ACAWGYAWAC WTTCTWWRYK
#1801      * * * * *

>AF269087      #1831      GAGCCTCCGG GGAAGCCATC TGCCTTCGAG
>BS322 1 to 1198 #18      AATCAT::TT TGCTTCCAAC :CCCATTAG
#1831      RAKCMTCCCK KGMWKCCAWC TSCCWTKAG
#1831      * * * * * * * * * *

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## BS322 Contig summary1.TXT

>AF269087	#1861	CCTGCCACTG	AAATGCAAAA	GTCTGTCCCA
>BS322 1 to 1198	#48	CCTGCCATTG	AAATGCAAAA	GTCTGTTCCA
	#1861	.....	.....	.....
		CCTGCCAYTG	AAATGCAAAA	GTCTGTYCCA
		*		*
>AF269087	#1891	AATAAAGCCT	TGGAATTGAA	AAATGAACAA
>BS322 1 to 1198	#78	AATAAAGCCT	TGGAATTGAA	GAATGAACAA
	#1891	.....	.....	.....
		AATAAAGCCT	TGGAATTGAA	RAATGAACAA
			*	
>AF269087	#1921	ACATGGAGAG	CAGATGAGAT	ACTCCCATCA
>BS322 1 to 1198	#108	ACATTGAGAG	CAGATGAGAT	ACTCCCATCA
	#1921	.....	.....	.....
		ACATKGAGAG	CAGATGAGAT	ACTCCCATCA
		*		
>AF269087	#1951	GAATCCAAAC	AAAAGGACTA	TGAAGAAAAT
>BS322 1 to 1198	#138	GAATCCAAAC	AAAAGGACTA	TGAAGAAAAGT
	#1951	.....	.....	.....
		GAATCCAAAC	AAAAGGACTA	TGAAGAAAAT
			*	
>AF269087	#1981	TCTTGGGATA	CTGAGAGTCT	CTGTGAGACT
>BS322 1 to 1198	#168	TCTTGGGATT	CTGAGAGTCT	CTGTGAGACT
	#1981	.....	.....	.....
		TCTTGGGATW	CTGAGAGTCT	CTGTGAGACT
		*		
>AF269087	#2011	GTTTCACAGA	AGGATGTGTG	TTTACCCAAG
>BS322 1 to 1198	#198	GTTTCACAGA	AGGATGTGTG	TTTACCCAAG
	#2011	.....	.....	.....
		GTTTCACAGA	AGGATGTGTG	TTTACCCAAG
>AF269087	#2041	GCTGCGCATC	AAAAAGAAAT	AGATAAAATA
>BS322 1 to 1198	#228	GCTGCGCATC	AAAAAGAAAT	AGATAAAATA
	#2041	.....	.....	.....
		GCTGCGCATC	AAAAAGAAAT	AGATAAAATA
>AF269087	#2071	AATGGAAAAT	TAGAAGGGTC	TCCTGTAAAA
>BS322 1 to 1198	#258	AATGGAAAAT	TAGAAGGGTC	TCCTGTAAAA
	#2071	.....	.....	.....
		AATGGAAAAT	TAGAAGGGTC	TCCTGTAAAA
>AF269087	#2101	GATGGTCTTC	TGAAGGCTAA	CTGCGGAATG
>BS322 1 to 1198	#288	GATGGTCTTC	TGAAGGCTAA	CTGCGGAATG
	#2101	.....	.....	.....
		GATGGTCTTC	TGAAGGCTAA	CTGCGGAATG
>AF269087	#2131	AAAGTTTCTA	TTCCAACATA	AGCCTTAGAA
>BS322 1 to 1198	#318	AAAGTTTCTA	TTCCAACATA	AGCCTTAGAA
	#2131	.....	.....	.....
		AAAGTTTCTA	TTCCAACATA	AGCCTTAGAA
>AF269087	#2161	TTGATGGACA	TGCAAACTTT	CAAAGCAGAG
>BS322 1 to 1198	#348	TTGATGGACA	TGCAAACTTT	CAAAGCAGAG
		.....	.....	.....

## BS322 Contig summary1.TXT

	#2161	TTGATGGACA TGCAAAC TTT CAAAGCAGAG
>AF269087	#2191	CCTCCCGAGA AGCCATCTGC CTTCGAGCCT
>BS322 1 to 1198	#378	CCTCCCGAGA AGCCATCTGC CTTCGAGCCT
	#2191	..... CCTCCCGAGA AGCCATCTGC CTTCGAGCCT
>AF269087	#2221	GCCATTGAAA TGCAAAAGTC TGTTCCAAAT
>BS322 1 to 1198	#408	GCCATTGAAA TGCAAAAGTC TGTTCCAAAT
	#2221	..... GCCATTGAAA TGCAAAAGTC TGTTCCAAAT
>AF269087	#2251	AAAGCCTTGG AATTGAAGAA TGAACAAACA
>BS322 1 to 1198	#438	AAAGCCTTGG AATTGAAGAA TGAACAAACA
	#2251	..... AAAGCCTTGG AATTGAAGAA TGAACAAACA
>AF269087	#2281	TTGAGAGCAG ATGAGATACT CCCATCAGAA
>BS322 1 to 1198	#468	TTGAGAGCAG ATGAGATACT CCCATCAGAA
	#2281	..... TTGAGAGCAG ATGAGATACT CCCATCAGAA
>AF269087	#2311	TCCAAACAAA AGGACTATGA AGAAAGTTCT
>BS322 1 to 1198	#498	TCCAAACAAA AGGACTATGA AGAAAGTTCT
	#2311	..... TCCAAACAAA AGGACTATGA AGAAAGTTCT
>AF269087	#2341	TGGGATTCTG AGAGTCTCTG TGAGACTGTT
>BS322 1 to 1198	#528	TGGGATTCTG AGAGTCTCTG TGAGACTGTT
	#2341	..... TGGGATTCTG AGAGTCTCTG TGAGACTGTT
>AF269087	#2371	TCACAGAAGG ATGTGTGTTT ACCCAAGGCT
>BS322 1 to 1198	#558	TCACAGAAGG ATGTGTGTTT ACCCAAGGCT
	#2371	..... TCACAGAAGG ATGTGTGTTT ACCCAAGGCT
>AF269087	#2401	ACACATCAAA AAGAAATAGA TAAAATAAAT
>BS322 1 to 1198	#588	ACACATCAAA AAGAAATAGA TAAAATAAAT
	#2401	..... ACACATCAAA AAGAAATAGA TAAAATAAAT
>AF269087	#2431	GGAAAATTAG AAGAGTCTCC TGATAATGAT
>BS322 1 to 1198	#618	GGAAAATTAG AAGAGTCTCC TGATAATGAT
	#2431	..... GGAAAATTAG AAGAGTCTCC TGATAATGAT
>AF269087	#2461	GGTTTTCTGA AGGCTCCCTG CAGAATGAAA
>BS322 1 to 1198	#648	GGTTTTCTGA AGGCTCCCTG CAGAATGAAA
	#2461	..... GGTTTTCTGA AGGCTCCCTG CAGAATGAAA

## BS322 Contig summary1.TXT

>AF269087	#2491	GTTTCTATTC CAACTAAAGC CTTAGAATTG
>BS322 1 to 1198	#678	GTTTCTATTC CAACTAAAGC CTTAGAATTG
	#2491	..... GTTTCTATTC CAACTAAAGC CTTAGAATTG
>AF269087	#2521	ATGGACATGC AAACCTTTCAA AGCAGAGCCT
>BS322 1 to 1198	#708	ATGGACATGC AAACCTTTCAA AGCAGAGCCT
	#2521	..... ATGGACATGC AAACCTTTCAA AGCAGAGCCT
>AF269087	#2551	CCCGAGAAGC CATCTGCCTT CGAGCCTGCC
>BS322 1 to 1198	#738	CCCGAGAAGC CATCTGCCTT CGAGCCTGCC
	#2551	..... CCCGAGAAGC CATCTGCCTT CGAGCCTGCC
>AF269087	#2581	ATTGAAATGC AAAAGTCTGT TCCAAATAAA
>BS322 1 to 1198	#768	ATTGAAATGC AAAAGTCTGT TCCAAATAAA
	#2581	..... ATTGAAATGC AAAAGTCTGT TCCAAATAAA
>AF269087	#2611	GCCTTGGAAT TGAAGAATGA ACAAACATTG
>BS322 1 to 1198	#798	GCCTTGGAAT TGAAGAATGA ACAAACATTG
	#2611	..... GCCTTGGAAT TGAAGAATGA ACAAACATTG
>AF269087	#2641	AGAGCAGATC AGATGTTCCC TTCAGAATCA
>BS322 1 to 1198	#828	AGAGCAGATC AGATGTTCCC TTCAGAATCA
	#2641	..... AGAGCAGATC AGATGTTCCC TTCAGAATCA
>AF269087	#2671	AAACAAAAGA AGGTTGAAGA AAATTCTTGG
>BS322 1 to 1198	#858	AAACAAAAGA ACGTTGAAGA AAATTCTTGG
	#2671	..... AAACAAAAGA ASGTTGAAGA AAATTCTTGG
		*
>AF269087	#2701	GATTCTGAGA GTCTCCGTGA GACTGTTTCA
>BS322 1 to 1198	#888	GATTCTGAGA GTCTCCGTGA GACTGTTTCA
	#2701	..... GATTCTGAGA GTCTCCGTGA GACTGTTTCA
>AF269087	#2731	CAGAAGGATG TGTGTGTACC CAAGGCTACA
>BS322 1 to 1198	#918	CAGAAGGATG TGTGTGTACC CAAGGCTACA
	#2731	..... CAGAAGGATG TGTGTGTACC CAAGGCTACA
>AF269087	#2761	CATCAAAAAG AAATGGATAA AATAAGTGGA
>BS322 1 to 1198	#948	CATCAAAAAG AAATGGATAA AATAAGTGGA
	#2761	..... CATCAAAAAG AAATGGATAA AATAAGTGGA
>AF269087	#2791	AAATTAGAAG ATTCAACTAG CCTATCAAAA
>BS322 1 to 1198	#978	AAATTAGAAG ATTCAACTAG CCTATCAAAA
		.....

## BS322 Contig summary1.TXT

	#2791	AAATTAGAAG ATTCAACTAG CCTATCAAAA
>AF269087	#2821	ATCTTGGATA CAGTTCATTG TTGTGAAAGA
>BS322 1 to 1198	#1008	ATCTTGGATA CAATTCATTG TTGTGAAAGA
	#2821	..... ATCTTGGATA CARTTCATTG TTGTGAAAGA *
>AF269087	#2851	GCAAGGGAAC TTCAAAAAGA TCACTGTGAA
>BS322 1 to 1198	#1038	GCAAGGGAAC TTCAAAAAGA TCACTGTGAA
	#2851	..... GCAAGGGAAC TTCAAAAAGA TCACTGTGAA
>AF269087	#2881	CAACGTACAG GAAAAATGGA ACAAATGAAA
>BS322 1 to 1198	#1068	CAATGTACAG GAAAAATGGA ACAAATGAAA
	#2881	..... CAAYGTACAG GAAAAATGGA ACAAATGAAA *
>AF269087	#2911	AAGAAGTTTT GTGTAAGTGA AAAGAAACTG
>BS322 1 to 1198	#1098	AAGAAGTTTT GTGTAAGTGA AAAGAAACTG
	#2911	..... AAGAAGTTTT GTGTAAGTGA AAAGAAACTG
>AF269087	#2941	TCAGAAGCAA AAGAAATAAA ATCACAGTTA
>BS322 1 to 1198	#1128	TCAGAAGCAA AAGAAATAAA ATCACAGTTA
	#2941	..... TCAGAAGCAA AAGAAATAAA ATCACAGTTA
>AF269087	#2971	GAGAACC AAAA AAGTTAAATG GGAACAAGAG
>BS322 1 to 1198	#1158	GAGAACC AAAA AAGTTAAATG GGAACAAGAG
	#2971	..... GAGAACC AAAA AAGTTAAATG GGAACAAGAG
>AF269087	#3001	CTCTGCAGTG TGAGATTGAC TTTAAACCAA
>BS322 1 to 1198	#1188	CTCTGCAGTG TGAG
	#3001	..... CTCTGCAGTG TGAGATTGAC TTTAAACCAA
>AF269087	#3031	GAAGAAGAGA AGAGAAGAAA TGCCGATATA
	#3031	..... GAAGAAGAGA AGAGAAGAAA TGCCGATATA
>AF269087	#3061	TTAAATGAAA AAATTAGGGA AGAATTAGGA
	#3061	..... TTAAATGAAA AAATTAGGGA AGAATTAGGA
>AF269087	#3091	AGAATCGAAG AGCAGCATAG GAAAGAGTTA
	#3091	..... AGAATCGAAG AGCAGCATAG GAAAGAGTTA
>AF269087	#3121	GAAGTGAAAC AACAACTTGA ACAGGCTCTC
	#3121	..... GAAGTGAAAC AACAACTTGA ACAGGCTCTC

## BS322 Contig summary1.TXT

>AF269087	#3151	AGAATACAAG ATATAGAATT GAAGAGTGTA
	#3151	AGAATACAAG ATATAGAATT GAAGAGTGTA
>BS322 1199 to 2683	>#1>	GT TTCTCACACT
>AF269087	#3181	GAAAGTAATT TGAATCAGGT TTCTCACACT
	#3181	GAAAGTAATT TGAATCAGGT TTCTCACACT
>BS322 1199 to 2683	#13	CATGAAAATG AAAATTATCT CTTACATGAA
>AF269087	#3211	CATGAAAATG AAAATTATCT CTTACATGAA
	#3211	CATGAAAATG AAAATTATCT CTTACATGAA
>BS322 1199 to 2683	#43	AATTGCATGT TGAAAAAGGA AATTGCCATG
>AF269087	#3241	AATTGCATGT TGAAAAAGGA AATTGCCATG
	#3241	AATTGCATGT TGAAAAAGGA AATTGCCATG
>BS322 1199 to 2683	#73	CTAAAACTGG AAATAGCCAC ACTGAAACAC
>AF269087	#3271	CTAAAACTGG AAATAGCCAC ACTGAAACAC
	#3271	CTAAAACTGG AAATAGCCAC ACTGAAACAC
>BS322 1199 to 2683	#103	CAATACCAGG AAAAGGAAAA TAAATACTTT
>AF269087	#3301	CAATACCAGG AAAAGGAAAA TAAATACTTT
	#3301	CAATACCAGG AAAAGGAAAA TAAATACTTT
>BS322 1199 to 2683	#133	GAGGACATTA AGATTTTAAA AGAAAAGAAT
>AF269087	#3331	GAGGACATTA AGATTTTAAA AGAAAAGAAT
	#3331	GAGGACATTA AGATTTTAAA AGAAAAGAAT
>BS322 1199 to 2683	#163	GCTGAACTTC AGATGACCCT AAAACTGAAA
>AF269087	#3361	GCTGAACTTC AGATGACCCT AAAACTGAAA
	#3361	GCTGAACTTC AGATGACCCT AAAACTGAAA
>BS322 1199 to 2683	#193	GAGGAATCAT TAACTAAAAG GGCATCTCAA
>AF269087	#3391	GAGGAATCAT TAACTAAAAG GGCATCTCAA
	#3391	GAGGAATCAT TAACTAAAAG GGCATCTCAA
>BS322 1199 to 2683	#223	TATAGTGGGC AGCTTAAAGT TCTGATAGCT
>AF269087	#3421	TATAGTGGGC AGCTTAAAGT TCTGATAGCT
	#3421	TATAGTGGGC AGCTTAAAGT TCTGATAGCT
>BS322 1199 to 2683	#253	GAGAACACAA TGCTCACTTC TAAATTGAAG
>AF269087	#3451	GAGAACACAA TGCTCACTTC TAAATTGAAG

## BS322 Contig summary1.TXT

```

#3451          .....
          GAGAACACAA TGCTCACTTC TAAATTGAAG

>BS322 1199 to 2683 #283      GAAAAACAAG ACAAAGAAAT ACTAGAGGCA
>AF269087          #3481      GAAAAACAAG ACAAAGAAAT ACTAGAGGCA
          #3481          .....
          GAAAAACAAG ACAAAGAAAT ACTAGAGGCA

>BS322 1199 to 2683 #313      GAAATTGAAT CACACCATCC TAGACTGGCT
>AF269087          #3511      GAAATTGAAT CACACCATCC TAGACTGGCT
          #3511          .....
          GAAATTGAAT CACACCATCC TAGACTGGCT

>BS322 1199 to 2683 #343      TCTGCTGTAC AAGACCATGA TCAAATTGTG
>AF269087          #3541      TCTGCTGTAC AAGACCATGA TCAAATTGTG
          #3541          .....
          TCTGCTGTAC AAGACCATGA TCAAATTGTG

>BS322 1199 to 2683 #373      ACATCAAGAA AAAGTCAAGA ACCTGCTTTC
>AF269087          #3571      ACATCAAGAA AAAGTCAAGA ACCTGCTTTC
          #3571          .....
          ACATCAAGAA AAAGTCAAGA ACCTGCTTTC

>BS322 1199 to 2683 #403      CACATTGCAG GAGATGCTTG TTTGCAAAGA
>AF269087          #3601      CACATTGCAG GAGATGCTTG TTTGCAAAGA
          #3601          .....
          CACATTGCAG GAGATGCTTG TTTGCAAAGA

>BS322 1199 to 2683 #433      AAAATGAATG TTGATGTGAG TAGTACGATA
>AF269087          #3631      AAAATGAATG TTGATGTGAG TAGTACGATA
          #3631          .....
          AAAATGAATG TTGATGTGAG TAGTACGATA

>BS322 1199 to 2683 #463      TATAACAATG AGGTGCTCCA TCAACCACTT
>AF269087          #3661      TATAACAATG AGGTGCTCCA TCAACCACTT
          #3661          .....
          TATAACAATG AGGTGCTCCA TCAACCACTT

>BS322 1199 to 2683 #493      TCTGAAGCTC AAAGGAAATC CAAAAGCCTA
>AF269087          #3691      TCTGAAGCTC AAAGGAAATC CAAAAGCCTA
          #3691          .....
          TCTGAAGCTC AAAGGAAATC CAAAAGCCTA

>BS322 1199 to 2683 #523      AAAATTAATC TCAATTATGC AGGAGATGCT
>AF269087          #3721      AAAATTAATC TCAATTATGC AGGAGATGCT
          #3721          .....
          AAAATTAATC TCAATTATGC AGGAGATGCT

>BS322 1199 to 2683 #553      CTAAGAGAAA ATACATTGGT TTCAGAACAT
>AF269087          #3751      CTAAGAGAAA ATACATTGGT TTCAGAACAT
          #3751          .....
          CTAAGAGAAA ATACATTGGT TTCAGAACAT

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BS322 Contig summary1.TXT

>BS322 1199 to 2683 #583	GCACAAAGAG ACCAACGTGA AACACAGTGT
>AF269087 #3781	GCACAAAGAG ACCAACGTGA AACACAGTGT
#3781	.....
	GCACAAAGAG ACCAACGTGA AACACAGTGT
>BS322 1199 to 2683 #613	CAAATGAAGG AAGCTGAACA CATGTATCAA
>AF269087 #3811	CAAATGAAGG AAGCTGAACA CATGTATCAA
#3811	.....
	CAAATGAAGG AAGCTGAACA CATGTATCAA
>BS322 1199 to 2683 #643	AACGAACAAG ATAATGTGAA CAAACACACT
>AF269087 #3841	AACGAACAAG ATAATGTGAA CAAACACACT
#3841	.....
	AACGAACAAG ATAATGTGAA CAAACACACT
>BS322 1199 to 2683 #673	GAACAGCAGG AGTCTCTAGA TCAGAAATTA
>AF269087 #3871	GAACAGCAGG AGTCTCTAGA TCAGAAATTA
#3871	.....
	GAACAGCAGG AGTCTCTAGA TCAGAAATTA
>BS322 1199 to 2683 #703	TTTCAACTAC AAAGCAAAAA TATGTGGCTT
>AF269087 #3901	TTTCAACTAC AAAGCAAAAA TATGTGGCTT
#3901	.....
	TTTCAACTAC AAAGCAAAAA TATGTGGCTT
>BS322 1199 to 2683 #733	CAACAGCAAT TAGTTCATGC ACATAAGAAA
>AF269087 #3931	CAACAGCAAT TAGTTCATGC ACATAAGAAA
#3931	.....
	CAACAGCAAT TAGTTCATGC ACATAAGAAA
>BS322 1199 to 2683 #763	GCTGACAACA AAAGCAAGAT AACCAATTGAT
>AF269087 #3961	GCTGACAACA AAAGCAAGAT AACCAATTGAT
#3961	.....
	GCTGACAACA AAAGCAAGAT AACCAATTGAT
>BS322 1199 to 2683 #793	ATTCATTTTC TTGAGAGGAA AATGCAACAT
>AF269087 #3991	ATTCATTTTC TTGAGAGGAA AATGCAACAT
#3991	.....
	ATTCATTTTC TTGAGAGGAA AATGCAACAT
>BS322 1199 to 2683 #823	CATCTCCTAA AAGAGAAAAA TGAGGAGATA
>AF269087 #4021	CATCTCCTAA AAGAGAAAAA TGAGGAGATA
#4021	.....
	CATCTCCTAA AAGAGAAAAA TGAGGAGATA
>BS322 1199 to 2683 #853	TTTAATTACA ATAACCATT TAAAAACCGT
>AF269087 #4051	TTTAATTACA ATAACCATT TAAAAACCGT
#4051	.....
	TTTAATTACA ATAACCATT TAAAAACCGT
>BS322 1199 to 2683 #883	ATATATCAAT ATGAAAAAGA GAAAGCAGAA
>AF269087 #4081	ATATATCAAT ATGAAAAAGA GAAAGCAGAA



## BS322 Contig summary1.TXT

```

#4081      .....
            ATATATCAAT ATGAAAAAGA GAAAGCAGAA

>BS322 1199 to 2683 #913      ACAGAAAAC T CATGAGAGAC AAGCAGTAAG
>AF269087      #4111      ACAGAAAAC T CATGAGAGAC AAGCAGTAAG
            .....
            ACAGAAAAC T CATGAGAGAC AAGCAGTAAG

>BS322 1199 to 2683 #943      AAACTTCTTT TGGAGAAACA ACAGACCAGA
>AF269087      #4141      AAACTTCTTT TGGAGAAACA ACAGACCAGA
            .....
            AAACTTCTTT TGGAGAAACA ACAGACCAGA

>BS322 1199 to 2683 #973      TCTTTACTCA CAACTCATGC TAGGAGGCCA
>AF269087      #4171      TCTTTACTCA CAACTCATGC TAGGAGGCCA
            .....
            TCTTTACTCA CAACTCATGC TAGGAGGCCA

>BS322 1199 to 2683 #1003     GTCCTAGCAT CACCTTATGT TGAAAATCTT
>AF269087      #4201      GTCCTAGCAT CACCTTATGT TGAAAATCTT
            .....
            GTCCTAGCAT CACCTTATGT TGAAAATCTT

>BS322 1199 to 2683 #1033     ACCAATAGTC TGTGTCAACA GAATACTTAT
>AF269087      #4231      ACCAATAGTC TGTGTCAACA GAATACTTAT
            .....
            ACCAATAGTC TGTGTCAACA GAATACTTAT

>BS322 1199 to 2683 #1063     TTTAGAAGAA AAATTCATGA TTTCTTCCTG
>AF269087      #4261      TTTAGAAGAA AAATTCATGA TTTCTTCCTG
            .....
            TTTAGAAGAA AAATTCATGA TTTCTTCCTG

>BS322 1199 to 2683 #1093     AAGCCTACAG ACATAAAATA ACAGTGTGAA
>AF269087      #4291      AAGCCTACAG ACATAAAATA ACAGTGTGAA
            .....
            AAGCCTACAG ACATAAAATA ACAGTGTGAA

>BS322 1199 to 2683 #1123     GAATTACTTG TTCACGAA:T :C:TCGCTCT
>AF269087      #4321      GAATTACTTG TTCACGAATT GCATAAAGCT
            .....
            GAATTACTTG TTCACGAATT GCATMRMKCT
                               * * * ****

>BS322 1199 to 2683 #1153     GCACTCCA:G CCTAGGCGCC TAGTGAAACC
>AF269087      #4351      GCACAGGATT CCCATCTACC CTGATGATGC
            .....
            GCACWSSATK CCYAKSYRCC YWGWKRAWSC
            *** ** * **** ** ** **

>BS322 1199 to 2683 #1183     CTGTGTCA:A AAAGAAAA:A AACAAAAACA
>AF269087      #4381      AGCAGACATC ATTCAATCCA ACCAGAATCT
            .....
            MKSWGWCATM AWWSAAWMCA AMCARAAWCW
            **** * ** *** ** * *

```

# BS322 Contig summary1.TXT

>BS322 1199 to 2683 #1213	AACT:TCCAA GAC:CTCGA: GTGGTTTTTG
>AF269087 #4411	CGCTCTGCAC TCCAGCCTAG GTGACAGAGT
#4411	.....
	MRCTCTSCAM KMCASYCKAG GTGRYWKWK
	** * * * ** ** * *
>BS322 1199 to 2683 #1243	GAGACCCTGT ATCACTTCAA ATAATGTGTT
>AF269087 #4441	GAGACTCCAC CTCGGAAA
#4441	.....
	GAGACYCYRY MTCRSWWMAA ATAATGTGTT
	* ** * *****
>BS322 1199 to 2683 #1273	AAACAAGCAT CTTCATCTCA TTAAATAGAA
#4471	.....
	AAACAAGCAT CTTCATCTCA TTAAATAGAA
>BS322 1199 to 2683 #1303	ATGTTGAAAA ATTGCTTTTG GAATAATTGA
#4501	.....
	ATGTTGAAAA ATTGCTTTTG GAATAATTGA
>BS322 1199 to 2683 #1333	CTTATGGATA TTTCATCAAA TTTACAGTTG
#4531	.....
	CTTATGGATA TTTCATCAAA TTTACAGTTG
>BS322 1199 to 2683 #1363	GCTATGCTTT CTTATTGTGC ATACTATGAA
#4561	.....
	GCTATGCTTT CTTATTGTGC ATACTATGAA
>BS322 1199 to 2683 #1393	ATGTTTTTCT TCAAAAAGTG TTTATAAGTG
#4591	.....
	ATGTTTTTCT TCAAAAAGTG TTTATAAGTG
>BS322 1199 to 2683 #1423	GTAAGTTTAA GAATGGGGTT GACAGCATT
#4621	.....
	GTAAGTTTAA GAATGGGGTT GACAGCATT
>BS322 1199 to 2683 #1453	TCTTTTGTGG TTATTTGATT AAACATTTAC
#4651	.....
	TCTTTTGTGG TTATTTGATT AAACATTTAC
>BS322 1199 to 2683 #1483	TAATTGTGCA TA
#4681	.....
	TAATTGTGCA TA

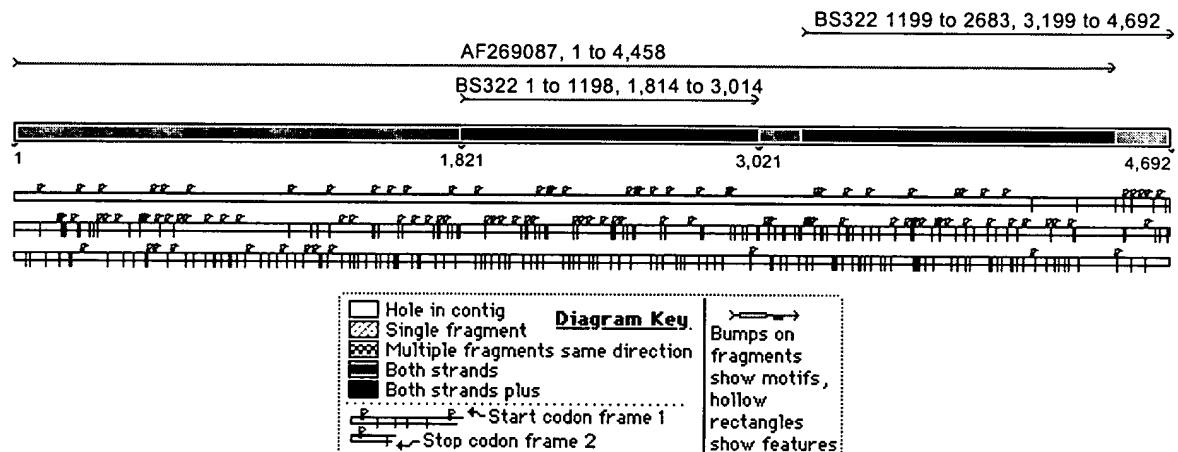
1. BS 322 contains 2683 nucleotides. This sequence was obtained by sequencing Incyte clone 4304443 in house.

2. NY-BR-1 (AF269087) contains 4466 nucleotides.

3. The contig (below) shows that BS322 is missing a single stretch of 185 nucleotides that are present in NY-BR-1. These nucleotides are missing between position 1198 and 1199 of BS322. The missing piece is nucleotides 3015 thru 3198 of NY-BR-1(AF269087). The first 45 bases of BS322 are a poor match to AF269087). The remaining bases are almost 100% identical. See BS322 contig summary file.

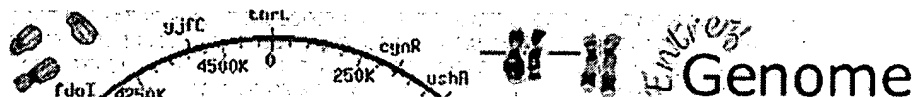
4. It appears that Incyte clone 4304443 is a splice variant of NY-BR-1. The gap occurs in the open reading frame region.

5. The primers used for the NY-BR-1 study were: Forward 2181 to 2202 and Reverse 3088 to 3111(AF269087). These primers are contained within BS322.





# results of BLAST



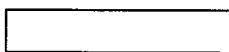
BLASTN 2.2.6 [Apr-09-2003]

RID: 1058379474-018463-9635

Database: contig

545 sequences; 2,866,452,029 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)



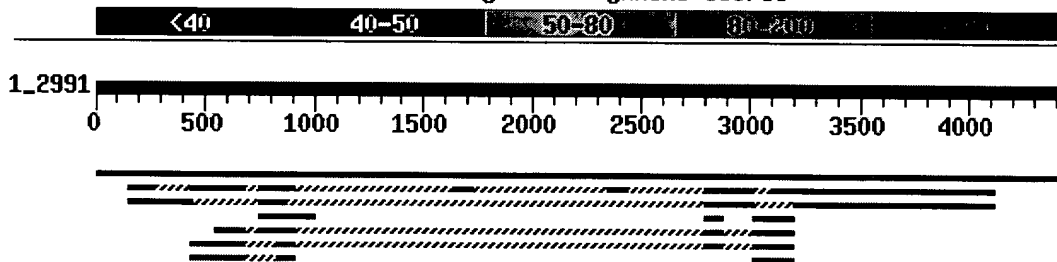
Show positions of the BLAST hits in the human genome using the Entrez  
Genomes MapViewer

Query= gi|13469728|gb|AF269087.1|AF269087 Homo sapiens breast  
cancer antigen NY-BR-1 mRNA, complete cds.  
(4458 letters)

Distribution of 115 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

## Color Key for Alignment Scores



Sequences producing significant alignments:

		Score	E
		(bits)	Value
ref NT_008705.14 Hs10_8862	Homo sapiens chromosome 10 genom...	1769	0.0
ref NT_011512.8 Hs21_11669	Homo sapiens chromosome 21 genom...	1319	0.0
ref NT_033985.5 Hs10_34140	Homo sapiens chromosome 10 genom...	1165	0.0
ref NT_011387.8 Hs20_11544	Homo sapiens chromosome 20 genom...	262	2e-66
ref NT_005058.13 Hs2_5215	Homo sapiens chromosome 2 genomic...	235	2e-58
ref NT_024983.9 Hs18_25139	Homo sapiens chromosome 18 genom...	202	1e-48
ref NT_078061.1 Hs9_78130	Homo sapiens chromosome 9 genomic...	192	1e-45
ref NT_078059.1 Hs9_78128	Homo sapiens chromosome 9 genomic...	192	1e-45
ref NT_037852.3 Hs15_37856	Homo sapiens chromosome 15 genom...	167	3e-38
ref NT_028395.2 Hs22_28554	Homo sapiens chromosome 22 genom...	127	5e-26

Alignments

>ref|NT\_008705.14|Hs10\_8862 Homo sapiens chromosome 10 genomic contig  
Length = 20794168

Score = 1769 bits (920), Expect = 0.0  
Identities = 920/920 (100%)  
Strand = Plus / Plus

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Sbjct: 19483239 aggtttctcacactcatgaaaatgaaaattatctcttacatgaaaattgcatgttgaaaa 19483298

Query: 3257 aggaaattgccatgctaaaactggaaatagccacactgaaacaccaataaccaggaaaaagg 3316  
|||||  
Sbjct: 19483299 aggaaattgccatgctaaaactggaaatagccacactgaaacaccaataaccaggaaaaagg 19483358

Query: 3317 aaaataaatactttgaggacattaagatttttaaagaaaagaatgctgaacttcagatga 3376  
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Sbjct: 19483359 aaaataaatactttgaggacattaagatttttaaagaaaagaatgctgaacttcagatga 19483418

Query: 3377 ccctaaaactgaaagaggaatcattaactaaaagggcattctcaatatagtgggcagctta 3436  
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Sbjct: 19483419 ccctaaaactgaaagaggaatcattaactaaaagggcattctcaatatagtgggcagctta 19483478

Query: 3437 aagttctgatagctgagaacacaatgctcacttctaattgaaggaaaaacaagacaaag 3496  
|||||  
Sbjct: 19483479 aagttctgatagctgagaacacaatgctcacttctaattgaaggaaaaacaagacaaag 19483538

Query: 3497 aaatactagaggcagaaattgaatcacaccatcctagactggcttctgctgtacaagacc 3556  
|||||  
Sbjct: 19483539 aaatactagaggcagaaattgaatcacaccatcctagactggcttctgctgtacaagacc 19483598

Query: 3557 atgatcaaattgtgacatcaagaaaaagtcaagaacctgctttccacattgcaggagatg 3616  
|||||  
Sbjct: 19483599 atgatcaaattgtgacatcaagaaaaagtcaagaacctgctttccacattgcaggagatg 19483658

Query: 3617 cttgtttgcaaagaaaaatgaatgttgatgtgagtagtacgatataacaatgaggtgc 3676  
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Sbjct: 19483659 cttgtttgcaaagaaaaatgaatgttgatgtgagtagtacgatataacaatgaggtgc 19483718

Query: 3677 tccatcaaccactttctgaagctcaaaggaaatccaaaagcctaaaaattaatctcaatt 3736  
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Sbjct: 19483719 tccatcaaccactttctgaagctcaaaggaaatccaaaagcctaaaaattaatctcaatt 19483778

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Sbjct: 19483839 gtgaaacacagtgtcaaatgaaggaagctgaacacatgtatcaaaacgaacaagataatg 19483898

Query: 3857 tgaacaaacacactgaacagcaggagtctctagatcagaaattatttcaactacaaagca 3916  
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Sbjct: 19483899 tgaacaaacacactgaacagcaggagtctctagatcagaaattatttcaactacaaagca 19483958

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Query: 3977 agataacaattgatattcattttcttgagaggaaaaatgcaacatcatctcctaaaagaga 4036  
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Sbjct: 19484019 agataacaattgatattcattttcttgagaggaaaaatgcaacatcatctcctaaaagaga 19484078

Query: 4037 aaaatgaggagatatttaattacaataaccattttaaaaaaccgtatatatcaatatgaaa 4096  
|||||  
Sbjct: 19484079 aaaatgaggagatatttaattacaataaccattttaaaaaaccgtatatatcaatatgaaa 19484138

Query: 4097 aagagaaagcagaaacagaa 4116  
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Sbjct: 19484139 aagagaaagcagaaacagaa 19484158

Score = 1108 bits (576), Expect = 0.0  
Identities = 576/576 (100%)  
Strand = Plus / Plus

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|||||  
Sbjct: 19405975 cagaaggaacatctgcaggaacacctgatgaggctgcacccttggcggaaagaacacctg 19406034

Query: 809 acacagctgaaagcttgggtggaaaaaacacctgatgaggctgcacccttgggtggaagaa 868  
|||||  
Sbjct: 19406035 acacagctgaaagcttgggtggaaaaaacacctgatgaggctgcacccttgggtggaagaa 19406094

Query: 869 cacctgacacggctgaaagcttgggtggaaaaaacacctgatgaggctgcaccccttgggtgg 928  
|||||  
Sbjct: 19406095 cacctgacacggctgaaagcttgggtggaaaaaacacctgatgaggctgcaccccttgggtgg 19406154

Query: 929 agggaaacatctgacaaaattcaatgtttggagaaagcgacatctggaaagtgcgaacagt 988  
|||||  
Sbjct: 19406155 agggaaacatctgacaaaattcaatgtttggagaaagcgacatctggaaagtgcgaacagt 19406214

Query: 989 cagcagaagaaacacctagggaaattacgagtcctgcaaaagaaacatctgagaaattta 1048  
|||||  
Sbjct: 19406215 cagcagaagaaacacctagggaaattacgagtcctgcaaaagaaacatctgagaaattta 19406274

Query: 1049 cgtggccagcaaaaggaagacctaggaagatcgcatgggagaaaaagaagacacaccta 1108  
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Sbjct: 19406275 cgtggccagcaaaaggaagacctaggaagatcgcatgggagaaaaagaagacacaccta 19406334

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Query: 1169 gacctaggaagatcgcatgggagaaaaaagaacacctgtaagactggatgcgtggcaa 1228  
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Sbjct: 19406395 gacctaggaagatcgcatgggagaaaaaagaacacctgtaagactggatgcgtggcaa 19406454

Query: 1229 gagtaacatctaataaaaactaaagtgttggaaaaaggaagatctaagatgattgcatgtc 1288  
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Query: 1289 ctacaaaagaatcatctacaaaagcaagtgccaatg 1324  
|||||

Sbjct: 19406515 ctacaaaagaatcatctacaaaagcaagtgccaatg 19406550

Score = 423 bits (220), Expect = e-115  
Identities = 220/220 (100%)  
Strand = Plus / Plus

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|||||  
Sbjct: 19495722 aactcatgagagacaagcagtaagaaacttcttttggagaaacaacagaccagatcttta 19495781

Query: 4177 ctcacaactcatgctaggaggccagtcctagcatcaccttatggtgaaaatcttaccaat 4236  
|||||  
Sbjct: 19495782 ctcacaactcatgctaggaggccagtcctagcatcaccttatggtgaaaatcttaccaat 19495841

Query: 4237 agtctgtgtcaacagaataacttattttagaagaaaaattcatgatttcttctgaagcct 4296  
|||||  
Sbjct: 19495842 agtctgtgtcaacagaataacttattttagaagaaaaattcatgatttcttctgaagcct 19495901

Query: 4297 acagacataaaaataacagtgtgaagaattacttggttcacg 4336  
|||||  
Sbjct: 19495902 acagacataaaaataacagtgtgaagaattacttggttcacg 19495941

Score = 415 bits (216), Expect = e-113  
Identities = 219/220 (99%), Gaps = 1/220 (0%)  
Strand = Plus / Plus

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||| |||||  
Sbjct: 19480436 agacagattcaactagcctatcaaaaatcttggatacagttcattcttgtgaaagagcaa 19480495

Query: 2855 gggaaacttcaaaaagatcactgtgaacaacgtacaggaaaaatggaacaaatgaaaaaga 2914  
|||||  
Sbjct: 19480496 gggaaacttcaaaaagatcactgtgaacaacgtacaggaaaaatggaacaaatgaaaaaga 19480555

Query: 2915 agttttgtgtactgaaaaagaaactgtcagaagcaaaagaaataaaatcacagttagaga 2974  
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Query: 2975 accaaaaagttaaatgggaacaagagctctgcagtgtgag 3014  
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Sbjct: 19480616 accaaaaagttaaatgggaacaagagctctgcagtgtgag 19480655

Score = 362 bits (188), Expect = 1e-96  
Identities = 188/188 (100%)  
Strand = Plus / Plus

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Query: 3073 attaggaagaattaggaagaatcgaagagcagcataggaaagagttagaagtgaacaa 3132  
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Sbjct: 19482014 attaggaagaattaggaagaatcgaagagcagcataggaaagagtagaagtgaacaa 19482073

Query: 3133 caacttgaacaggctctcagaatacaagatatagaattgaagagtgtagaaagtaatttg 3192  
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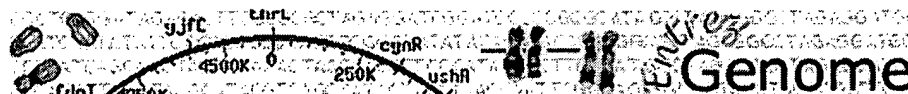
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Sbjct: 19482134 aatcaggt 19482141





# results of BLAST



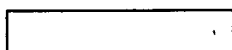
BLASTN 2.2.6 [Apr-09-2003]

RID: 1058379474-018463-9635

Database: contig

545 sequences; 2,866,452,029 total letters

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQs](#)



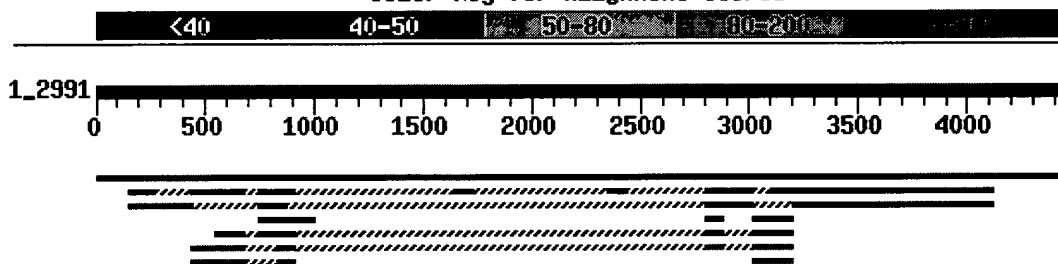
Show positions of the BLAST hits in the human genome using the Entrez  
Genomes MapViewer

Query= gi|13469728|gb|AF269087.1|AF269087 Homo sapiens breast  
cancer antigen NY-BR-1 mRNA, complete cds.  
(4458 letters)

Distribution of 115 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments

Color Key for Alignment Scores



Sequences producing significant alignments:

		Score (bits)	E Value
ref NT_008705.14 Hs10_8862	Homo sapiens chromosome 10 genom...	1769	0.0
ref NT_011512.8 Hs21_11669	Homo sapiens chromosome 21 genom...	1319	0.0
ref NT_033985.5 Hs10_34140	Homo sapiens chromosome 10 genom...	1165	0.0
ref NT_011387.8 Hs20_11544	Homo sapiens chromosome 20 genom...	262	2e-66
ref NT_005058.13 Hs2_5215	Homo sapiens chromosome 2 genomic...	235	2e-58
ref NT_024983.9 Hs18_25139	Homo sapiens chromosome 18 genom...	202	1e-48
ref NT_078061.1 Hs9_78130	Homo sapiens chromosome 9 genomic...	192	1e-45
ref NT_078059.1 Hs9_78128	Homo sapiens chromosome 9 genomic...	192	1e-45
ref NT_037852.3 Hs15_37856	Homo sapiens chromosome 15 genom...	167	3e-38
ref NT_028395.2 Hs22_28554	Homo sapiens chromosome 22 genom...	127	5e-26

Alignments

>ref|NT\_008705.14|Hs10\_8862 Homo sapiens chromosome 10 genomic contig  
Length = 20794168

Score = 1769 bits (920), Expect = 0.0  
Identities = 920/920 (100%)  
Strand = Plus / Plus

Query: 3197 aggtttctcacactcatgaaaatgaaaattatctcttacatgaaaattgcatgttgaaaa 3256  
|||||  
Sbjct: 19483239 aggtttctcacactcatgaaaatgaaaattatctcttacatgaaaattgcatgttgaaaa 19483298

Query: 3257 aggaaattgccatgctaaaactggaaatagccacactgaaacaccaataaccaggaaaagg 3316  
|||||  
Sbjct: 19483299 aggaaattgccatgctaaaactggaaatagccacactgaaacaccaataaccaggaaaagg 19483358

Query: 3317 aaaataaatactttgaggacattaagattttaaaagaaaagaatgctgaacttcagatga 3376  
|||||  
Sbjct: 19483359 aaaataaatactttgaggacattaagattttaaaagaaaagaatgctgaacttcagatga 19483418

Query: 3377 ccctaaaactgaaagaggaatcattaactaaaagggcatctcaatatagtgggcagctta 3436  
|||||  
Sbjct: 19483419 ccctaaaactgaaagaggaatcattaactaaaagggcatctcaatatagtgggcagctta 19483478

Query: 3437 aagttctgatagctgagaacacaatgctcacttctaaattgaaggaaaaacaagacaaag 3496  
|||||  
Sbjct: 19483479 aagttctgatagctgagaacacaatgctcacttctaaattgaaggaaaaacaagacaaag 19483538

Query: 3497 aaatactagaggcagaaattgaatcacaccatcctagactggcttctgctgtacaagacc 3556  
|||||  
Sbjct: 19483539 aaatactagaggcagaaattgaatcacaccatcctagactggcttctgctgtacaagacc 19483598

Query: 3557 atgatcaaattgtgacatcaagaaaaagtcaagaacctgctttccacattgcaggagatg 3616  
|||||  
Sbjct: 19483599 atgatcaaattgtgacatcaagaaaaagtcaagaacctgctttccacattgcaggagatg 19483658

Query: 3617 cttgtttgcaaagaaaaatgaatgttgatgtgagtagtacgatataatacaatgaggtgc 3676  
|||||  
Sbjct: 19483659 cttgtttgcaaagaaaaatgaatgttgatgtgagtagtacgatataatacaatgaggtgc 19483718

Query: 3677 tccatcaaccactttctgaagctcaaaggaaatccaaaagcctaaaaattaatctcaatt 3736  
|||||  
Sbjct: 19483719 tccatcaaccactttctgaagctcaaaggaaatccaaaagcctaaaaattaatctcaatt 19483778

Query: 3737 atgcaggagatgctctaagagaaaatacattgggttcagaacatgcacaaagagaccaac 3796  
|||||  
Sbjct: 19483779 atgcaggagatgctctaagagaaaatacattgggttcagaacatgcacaaagagaccaac 19483838

Query: 3797 gtgaaacacagtgtcaaataaggaagctgaacacatgtatcaaacgaacaagataatg 3856  
|||||  
Sbjct: 19483839 gtgaaacacagtgtcaaataaggaagctgaacacatgtatcaaacgaacaagataatg 19483898

Query: 3857 tgaacaaacacactgaacagcaggagtctctagatcagaaattatttcaactacaaagca 3916  
|||||  
Sbjct: 19483899 tgaacaaacacactgaacagcaggagtctctagatcagaaattatttcaactacaaagca 19483958

Query: 3917 aaaatatgtggcttcaacagcaattagttcatgcacataagaaagctgacaacaaaagca 3976  
|||||  
Sbjct: 19483959 aaaatatgtggcttcaacagcaattagttcatgcacataagaaagctgacaacaaaagca 19484018

Query: 3977 agataacaattgatattcattttcttgagaggaaaatgcaacatcatctcctaaaagaga 4036  
|||||  
Sbjct: 19484019 agataacaattgatattcattttcttgagaggaaaatgcaacatcatctcctaaaagaga 19484078

Query: 4037 aaaatgaggagatatttaattacaataaccatttaaaaaaccgtatatatcaatatgaaa 4096  
|||||  
Sbjct: 19484079 aaaatgaggagatatttaattacaataaccatttaaaaaaccgtatatatcaatatgaaa 19484138

Query: 4097 aagagaaagcagaaacagaa 4116  
|||||  
Sbjct: 19484139 aagagaaagcagaaacagaa 19484158

Score = 1108 bits (576), Expect = 0.0  
Identities = 576/576 (100%)  
Strand = Plus / Plus

Query: 749 cagaaggaacatctgcaggaacacctgatgaggctgcacccttggcggaaagaacacctg 808  
|||||  
Sbjct: 19405975 cagaaggaacatctgcaggaacacctgatgaggctgcacccttggcggaaagaacacctg 19406034

Query: 809 acacagctgaaagcttggtggaaaaaacacctgatgaggctgcacccttggaggaaagaa 868  
|||||  
Sbjct: 19406035 acacagctgaaagcttggtggaaaaaacacctgatgaggctgcacccttggaggaaagaa 19406094

Query: 869 cacctgacacggctgaaagcttggtggaaaaaacacctgatgaggctgcatccttggtgg 928  
|||||  
Sbjct: 19406095 cacctgacacggctgaaagcttggtggaaaaaacacctgatgaggctgcatccttggtgg 19406154

Query: 929 agggaaacatctgacaaaattcaatgtttggagaaagcgacatctggaaagttcgaacagt 988  
|||||  
Sbjct: 19406155 agggaaacatctgacaaaattcaatgtttggagaaagcgacatctggaaagttcgaacagt 19406214

Query: 989 cagcagaagaaacacctagggaaattacgagtcctgcaaaagaaacatctgagaaattta 1048  
|||||  
Sbjct: 19406215 cagcagaagaaacacctagggaaattacgagtcctgcaaaagaaacatctgagaaattta 19406274

Query: 1049 cgtggccagcaaaaggaagacctaggaagatcgcatgggagaaaaagaagacacaccta 1108  
|||||  
Sbjct: 19406275 cgtggccagcaaaaggaagacctaggaagatcgcatgggagaaaaagaagacacaccta 19406334

Query: 1109 gggaaattatgagtcgcaaaagaaacatctgagaaatttacgtgggcagcaaaaggaa 1168  
|||||  
Sbjct: 19406335 gggaaattatgagtcgcaaaagaaacatctgagaaatttacgtgggcagcaaaaggaa 19406394

Query: 1169 gacctaggaagatcgcatgggagaaaaaagaaacacctgtaagactggatgcgtggcaa 1228  
|||||  
Sbjct: 19406395 gacctaggaagatcgcatgggagaaaaaagaaacacctgtaagactggatgcgtggcaa 19406454

Query: 1229 gagtaacatctaataaaactaaagtgtttggaaaaaggaagatctaagatgattgcatgtc 1288  
|||||  
Sbjct: 19406455 gagtaacatctaataaaactaaagtgtttggaaaaaggaagatctaagatgattgcatgtc 19406514

Query: 1289 ctacaaaagaatcatctacaaaagcaagtgccaatg 1324  
|||||

Sbjct: 19406515 ctacaaaagaatcatctacaaaagcaagtgccaatg 19406550

Score = 423 bits (220), Expect = e-115  
Identities = 220/220 (100%)  
Strand = Plus / Plus

Query: 4117 aactcatgagagacaagcagtaagaaacttcttttggagaacaacagaccagatcttta 4176  
|||||  
Sbjct: 19495722 aactcatgagagacaagcagtaagaaacttcttttggagaacaacagaccagatcttta 19495781

Query: 4177 ctcacaactcatgctaggaggccagtcctagcatcaccttatgttgaaaatcttaccat 4236  
|||||  
Sbjct: 19495782 ctcacaactcatgctaggaggccagtcctagcatcaccttatgttgaaaatcttaccat 19495841

Query: 4237 agtctgtgtcaacagaataacttattttagaagaaaaattcatgatttcttcctgaagcct 4296  
|||||  
Sbjct: 19495842 agtctgtgtcaacagaataacttattttagaagaaaaattcatgatttcttcctgaagcct 19495901

Query: 4297 acagacataaaataacagtgtgaagaattacttggtcacg 4336  
|||||  
Sbjct: 19495902 acagacataaaataacagtgtgaagaattacttggtcacg 19495941

Score = 415 bits (216), Expect = e-113  
Identities = 219/220 (99%), Gaps = 1/220 (0%)  
Strand = Plus / Plus

Query: 2796 aga-agattcaactagcctatcaaaaatcttggatacagttcattcttgtgaaagagcaa 2854  
|||  
Sbjct: 19480436 agacagattcaactagcctatcaaaaatcttggatacagttcattcttgtgaaagagcaa 19480495

Query: 2855 gggaaacttcaaaaagatcactgtgaacaacgtacaggaaaaatggaacaaatgaaaaaga 2914  
|||||  
Sbjct: 19480496 gggaaacttcaaaaagatcactgtgaacaacgtacaggaaaaatggaacaaatgaaaaaga 19480555

Query: 2915 agttttgtgtactgaaaaagaaactgtcagaagcaaaagaaataaaatcacagttagaga 2974  
|||||  
Sbjct: 19480556 agttttgtgtactgaaaaagaaactgtcagaagcaaaagaaataaaatcacagttagaga 19480615

Query: 2975 accaaaaagttaaattgggaacaagagctctgcagtgtgag 3014  
|||||  
Sbjct: 19480616 accaaaaagttaaattgggaacaagagctctgcagtgtgag 19480655

Score = 362 bits (188), Expect = 1e-96  
Identities = 188/188 (100%)  
Strand = Plus / Plus

Query: 3013 agattgacttttaaccaagaagaagagaagagaagaaatgccgatattataatgaaaaa 3072  
|||||  
Sbjct: 19481954 agattgacttttaaccaagaagaagagaagagaagaaatgccgatattataatgaaaaa 19482013

Query: 3073 attaggaagaattaggaagaatcgaagagcagcataggaaagagttagaagtgaacaa 3132  
|||||

Sbjct: 19482014 attaggaagaattaggaagaatcgaagagcagcataggaaagagttagaagtgaacaa 19482073

Query: 3133 caacttgaacaggctctcagaatacaagatatagaattgaagagtgtagaaagtaatttg 3192

|||||

Sbjct: 19482074 caacttgaacaggctctcagaatacaagatatagaattgaagagtgtagaaagtaatttg 19482133

Query: 3193 aatcaggt 3200

|||||

Sbjct: 19482134 aatcaggt 19482141